

#7

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RAW SEQUENCE LISTING  
PATENT APPLICATION: US/09/747,155

DATE: 08/16/2001  
TIME: 13:54:51

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Output Set: N:\CRF3\08162001\I747155.raw

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3 <110> APPLICANT: Rouquier, Sylvie  
4 Giorgi, Dominique  
6 <120> TITLE OF INVENTION: Novel Polypeptides and Nucleic Acids Encoding Same  
8 <130> FILE REFERENCE: 19904-008 (C009B6834US)  
10 <140> CURRENT APPLICATION NUMBER: 09/747,155  
11 <141> CURRENT FILING DATE: 2000-12-21  
13 <150> PRIOR APPLICATION NUMBER: 60/171,746  
14 <151> PRIOR FILING DATE: 1999-12-22  
16 <160> NUMBER OF SEQ ID NOS: 431  
18 <170> SOFTWARE: PatentIn version 3.0  
20 <210> SEQ ID NO: 1  
21 <211> LENGTH: 649  
22 <212> TYPE: DNA  
23 <213> ORGANISM: Papio hamadryas  
25 <220> FEATURE:  
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27 <222> LOCATION: (1)..(649)  
28 <223> OTHER INFORMATION: Taxon = 9557; gene = PPA13; Accession DDBJ/EMBL/GenBank =  
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30 <220> FEATURE:  
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32 <222> LOCATION: (2)..(649)  
33 <223> OTHER INFORMATION: Product = olfactory receptor  
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38 1 5 10 15  
40 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc 97  
41 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr  
42 20 25 30  
44 cag gtc tat ttc tcc atg ttt ttt cct att ctg ggc aca cta ctc ctg 145  
45 Gln Val Tyr Phe Ser Met Phe Pro Ile Leu Gly Thr Leu Leu Leu  
46 35 40 45  
48 acc gtg atg gcc tat gac cgg ttt gtg gcc gtc tgc cac ccc ctg cac 193  
49 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His  
50 50 55 60  
52 tat ata acc atc atg aac ccc cgc ctc tgt ggc ctc ctg gtt ttt gtc 241  
53 Tyr Ile Thr Ile Met Asn Pro Arg Leu Cys Gly Leu Leu Val Phe Val  
54 65 70 75 80  
56 acg tgg ctc att ggt gtc atg acg tcc ctc ctc cat att tct ctg atg 289  
57 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met  
58 85 90 95  
60 aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337  
61 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys  
62 100 105 110  
64 gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385  
65 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn  
66 115 120 125

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68	agc	acg	ttg	ata	tat	gtt	atg	acg	ggt	gtg	ctg	ggc	gtt	ttt	ccc	ctc	433
69	Ser	Thr	Leu	Ile	Tyr	Val	Met	Thr	Gly	Val	Leu	Gly	Val	Phe	Pro	Leu	
70	130				135						140						
72	ctt	ggg	atc	att	ttc	tct	tat	tca	cga	atc	gct	tca	tcc	ata	agg	aag	481
73	Leu	Gly	Ile	Ile	Phe	Ser	Tyr	Ser	Arg	Ile	Ala	Ser	Ser	Ile	Arg	Lys	
74	145				150				155		160						
76	atg	tcc	tca	tct	ggg	gga	aaa	gag	aaa	gca	ctt	tct	acc	tgt	ggc	tct	529
77	Met	Ser	Ser	Gly	Gly	Lys	Glu	Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser		
78	165				170					175							
80	cac	ctc	tcc	gtc	gtt	tct	tta	ttt	tat	ggg	aca	ggc	att	ggg	gtc	cac	577
81	His	Leu	Ser	Val	Val	Ser	Leu	Phe	Tyr	Gly	Thr	Gly	Ile	Gly	Val	His	
82	180				185					190							
84	ttc	act	tct	gcg	gtg	act	cat	tct	tcc	cag	aac	atc	tcc	gtg	gcc	tcg	625
85	Phe	Thr	Ser	Ala	Val	Thr	His	Ser	Ser	Gln	Asn	Ile	Ser	Val	Ala	Ser	
86	195				200					205							
88	gtg	atg	tac	acg	gtg	gtt	acc	ccc									649
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108	Asn	Ile	Gln	Thr	Lys	Asn	Lys	Thr	Ile	Ser	Tyr	Met	Asp	Cys	Leu	Thr	
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112	Gln	Val	Tyr	Phe	Ser	Met	Phe	Phe	Pro	Ile	Leu	Gly	Thr	Leu	Leu	Leu	
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116	Thr	Val	Met	Ala	Tyr	Asp	Arg	Phe	Val	Ala	Val	Cys	His	Pro	Leu	His	
117					50			55				60					
120	Tyr	Ile	Thr	Ile	Met	Asn	Pro	Arg	Leu	Cys	Gly	Leu	Leu	Val	Phe	Val	
121					65			70			75			80			
124	Thr	Trp	Leu	Ile	Gly	Val	Met	Thr	Ser	Leu	Leu	His	Ile	Ser	Leu	Met	
125					85				90			95					
128	Thr	His	Leu	Thr	Phe	Cys	Lys	Asp	Phe	Glu	Ile	Pro	His	Phe	Phe	Cys	
129					100			105			110						
132	Glu	Leu	Thr	His	Ile	Leu	Gln	Leu	Ala	Cys	Ser	Asp	Thr	Phe	Leu	Asn	
133					115			120			125						
136	Ser	Thr	Leu	Ile	Tyr	Val	Met	Thr	Gly	Val	Leu	Gly	Val	Phe	Pro	Leu	
137					130			135			140						
140	Leu	Gly	Ile	Ile	Phe	Ser	Tyr	Ser	Arg	Ile	Ala	Ser	Ser	Ile	Arg	Lys	
141					145			150			155			160			
144	Met	Ser	Ser	Ser	Gly	Gly	Lys	Glu	Lys	Ala	Leu	Ser	Thr	Cys	Gly	Ser	
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Input Set : A:\Breeese-1.app  
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148 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His  
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152 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser  
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156 Val Met Tyr Thr Val Val Thr Pro  
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175 cgcatgtatg gaaagtctgc tcctggctgt gatggcctat gaccggtttggccatctg 180  
177 tcacccctca cactgccag tcactcatgaa cccacgcctt tggcctttt tagttttgg 240  
179 gtcttttctt cttagcctgt tggattccca gctacacaat ttgattgtgt tacaacttac 300  
181 ctgcttcaat gatgtggaaa tctctaaatt tttctgtgac ccttctcaac ttctcaatcc 360  
183 tagcctgctc tgacacataa catagtcgta tattttattt gtaccatatt tggttttctt 420  
185 cctctctcag ggatcctttt cttttactat aaaattgttt cctccatcc gagagttcgc 480  
187 tcttcaggta ggaagtataa agccttctcc acctgcagct ctcacccctt agttgtttgc 540  
189 ttattttatg gaacagccct tggagggtagt ctcagttcag ctgtctctt cccccccagg 600  
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212 1 5 10 15  
214 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc 97  
215 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr  
216 20 25 30  
218 cag gtc tat ttc tcc atg ttt cct att ctg gac aca cta ctc ctg 145  
219 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu  
220 35 40 45  
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 228 65 70 75 80  
 230 acg tgg ctc att ggt gtc atg aca tcc ctc cat att tct ctg atg 289  
 231 Thr Trp Leu Ile Gly Val Met Thr Ser Leu Leu His Ile Ser Leu Met  
 232 85 90 95  
 234 aca cat cta acc ttc tgt aaa gat ttt gaa att cca cat ttt ttc tgc 337  
 235 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys  
 236 100 105 110  
 238 gaa ctg aca cat atc ctc cag ctg gcc tgc tct gat acc ttc ctg aac 385  
 239 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn  
 240 115 120 125  
 242 agc acg ttg ata tat gtt atg acg ggt gtg ctg ggc gtt ttt ccc ctc 433  
 243 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu  
 244 130 135 140  
 246 ctt ggg atc att ttc tct tat tca cga atc gct tca tcc ata agg aag 481  
 247 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys  
 248 145 150 155 160  
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 252 165 170 175  
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 256 180 185 190  
 258 ttc act tct gcg gtg act cat tct tcc cag aac atc tcc gtg gcc tcg 625  
 259 Phe Thr Ser Ala Val Thr His Ser Ser Gln Asn Ile Ser Val Ala Ser  
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 279 1 5 10 15  
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 283 20 25 30  
 286 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu Leu  
 287 35 40 45  
 290 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Val Cys His Pro Leu His  
 291 50 55 60

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302 Thr His Leu Thr Phe Cys Lys Asp Phe Glu Ile Pro His Phe Phe Cys  
303 100 105 110  
306 Glu Leu Thr His Ile Leu Gln Leu Ala Cys Ser Asp Thr Phe Leu Asn  
307 115 120 125  
310 Ser Thr Leu Ile Tyr Val Met Thr Gly Val Leu Gly Val Phe Pro Leu  
311 130 135 140  
314 Leu Gly Ile Ile Phe Ser Tyr Ser Arg Ile Ala Ser Ser Ile Arg Lys  
315 145 150 155 160  
318 Met Ser Ser Ser Gly Gly Lys Glu Lys Ala Leu Ser Thr Cys Gly Ser  
319 165 170 175  
322 His Leu Ser Val Val Ser Leu Phe Tyr Gly Thr Gly Ile Gly Val His  
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327 195 200 205  
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352 1 5 10 15  
354 aac atc cag acc aag aac aaa acg att tct tac atg gac tgc ctc acc 97  
355 Asn Ile Gln Thr Lys Asn Lys Thr Ile Ser Tyr Met Asp Cys Leu Thr  
356 20 25 30  
358 cag gtc tat ttc tcc atg ttt cct att ctg gac aca cta ctc ctg 145  
359 Gln Val Tyr Phe Ser Met Phe Phe Pro Ile Leu Asp Thr Leu Leu  
360 35 40 45  
362 acc gtg atg gcc tat gac cgg ttt gtg gcc atc tat cac tcc ctg cac 193  
363 Thr Val Met Ala Tyr Asp Arg Phe Val Ala Ile Tyr His Ser Leu His  
364 50 55 60  
366 tac acg gtc atc atg agc ccc cgg ctc tgt gga ctg ctg gtt ctg gga 241  
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**VERIFICATION SUMMARY**

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